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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/714,767

DATE: 12/01/2000

TIME: 13:32:14

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\12012000\I714767.raw

```

4 <110> APPLICANT: Bidney, Dennis
5   Duvick, Jon
6   Hendrick, Carol
7   Hu, Xu
8   Lu, Guihua
9   Crasta, Oswald
12 <120> TITLE OF INVENTION: Sunflower RhoGAP, LOX, ADH and SCIP -
13   Polynucleotides and Methods of Use
16 <130> FILE REFERENCE: 35718/201902
C--> 18 <140> CURRENT APPLICATION NUMBER: US/09/714,767
C--> 18 <141> CURRENT FILING DATE: 2000-11-16
18 <150> PRIOR APPLICATION NUMBER: US 60/166,128
19 <151> PRIOR FILING DATE: 1999-11-18
21 <150> PRIOR APPLICATION NUMBER: US 60/201,837
22 <151> PRIOR FILING DATE: 2000-05-03
24 <160> NUMBER OF SEQ ID NOS: 10
26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 824
30 <212> TYPE: DNA
31 <213> ORGANISM: Helianthus annuus
33 <220> FEATURE:
34 <221> NAME/KEY: misc_feature
35 <222> LOCATION: (0)...(0)
36 <223> OTHER INFORMATION: rhoGAP
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (35)...(637)
41 <400> SEQUENCE: 1
42 ttgggcacga gtccaaatcc aatcttcaat cacc atg gct gaa gaa caa ctg ccg      55
43                                     1       5
44                                     Met Ala Glu Glu Gln Leu Pro
46 cct gat caa att aaa ctc att cac aag ctt aat ttg ttc aaa atc aaa      103
47 Pro Asp Gln Ile Lys Leu Ile His Lys Leu Asn Leu Phe Lys Ile Lys
48   10       15       20
50 ggc aga gat aaa cac aat cgc aaa atc tta cga att gtc gga aaa aac      151
51 Gly Arg Asp Lys His Asn Arg Lys Ile Leu Arg Ile Val Gly Lys Asn
52   25       30       35
54 ttt cca gct aag agt ttg acc gtt gac ctg ttg aaa aaa tat cta gaa      199
55 Phe Pro Ala Lys Ser Leu Thr Val Asp Leu Leu Lys Lys Tyr Leu Glu
56  40       45       50       55
58 gtg aaa att ttc ccc aaa ctt gaa cga ccg ttt gtg gtg gtt tac gtt      247
59 Val Lys Ile Phe Pro Lys Leu Glu Arg Pro Phe Val Val Val Tyr Val
60   60       65       70
62 cac act gat gtt cag aag agc gag aat ttc cct gga ata tcc gtt ctc      295
63 His Thr Asp Val Gln Lys Ser Glu Asn Phe Pro Gly Ile Ser Val Leu
64   75       80       85
66 cgg tca gtt tac gac gcg att ccg atg acc gtg aaa caa tat ctt gag      343

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```

67 Arg Ser Val Tyr Asp Ala Ile Pro Met Thr Val Lys Gln Tyr Leu Gln
68          90          95          100
70 gcg gtt tac ttt gtt cat ccg gat ctg cag tcc aga att ttt ctg gct      391
71 Ala Val Tyr Phe Val His Pro Asp Leu Gln Ser Arg Ile Phe Leu Ala
72          105          110          115
74 aca ttt ggc cgg ctt atc ttc acc gga ggg tta tat gca aag ctg aga      439
75 thr Phe Gly Arg Leu Ile Phe Thr Gly Gly Leu Tyr Ala Lys Leu Arg
76 120          125          130          135
78 ttt gtg agt cga ttg gcg tat ctg tgg gaa cat gtg aaa agg aac gag      487
79 Phe Val Ser Arg Leu Ala Tyr Leu Trp Glu His Val Lys Arg Asn Glu
80          140          145          150
82 atc gag atc cca gag ttt gtc tac gat cat gat gag gat ctg gag tac      535
83 Ile Glu Ile Pro Glu Phe Val Tyr Asp His Asp Glu Asp Leu Glu Tyr
84          155          160          165
86 cgt ccg atg atg gat tac ggg ata gag agt gac cac gct aga gtt tat      583
87 Arg Pro Met Met Asp Tyr Gly Ile Glu Ser Asp His Ala Arg Val Tyr
88          170          175          180
90 gga gcg ccc gcg gtt gat tcc tct gtg gcg gct tat tcc atg agg tgt      631
91 Gly Ala Pro Ala Val Asp Ser Ser Val Ala Ala Tyr Ser Met Arg Cys
92          185          190          195
94 atc tca taggggaaat agttgttttt tcttttgttt ttgaaaatag gtgctaaaag      687
95 Ile Ser
96 200
98 aagtccaata tatagtattt agcaatatatt cgggtgttgt agtatgttga taacgggctt      747
99 ttcttataac attcattggt ctagttttct ttgtataaaa ttatttgata aattctttgt      807
100 aaaaaaaaaa aaaaaaa
102 <210> SEQ ID NO: 2
103 <211> LENGTH: 201
104 <212> TYPE: PRT
105 <213> ORGANISM: Helianthus annuus
107 <400> SEQUENCE: 2
108 Met Ala Glu Glu Gln Leu Pro Pro Asp Gln Ile Lys Leu Ile His Lys
109 1 5 10 15
110 Leu Asn Leu Phe Lys Ile Lys Gly Arg Asp Lys His Asn Arg Lys Ile
111 20 25 30
112 Leu Arg Ile Val Gly Lys Asn Phe Pro Ala Lys Ser Leu Thr Val Asp
113 35 40 45
114 Leu Leu Lys Lys Tyr Leu Glu Val Lys Ile Phe Pro Lys Leu Glu Arg
115 50 55 60
116 Pro Phe Val Val Val Tyr Val His Thr Asp Val Gln Lys Ser Glu Asn
117 65 70 75 80
118 Phe Pro Gly Ile Ser Val Leu Arg Ser Val Tyr Asp Ala Ile Pro Met
119 85 90 95
120 Thr Val Lys Gln Tyr Leu Glu Ala Val Tyr Phe Val His Pro Asp Leu
121 100 105 110
122 Gln Ser Arg Ile Phe Leu Ala Thr Phe Gly Arg Leu Ile Phe Thr Gly
123 115 120 125
124 Gly Leu Tyr Ala Lys Leu Arg Phe Val Ser Arg Leu Ala Tyr Leu Trp
125 130 135 140

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```

126 Glu His Val Lys Arg Asn Glu Ile Glu Ile Pro Glu Phe Val Tyr Asp
127 145 150 155 160
128 His Asp Glu Asp Leu Glu Tyr Arg Pro Met Met Asp Tyr Gly Ile Glu
129 165 170 175
130 Ser Asp His Ala Arg Val Tyr Gly Ala Pro Ala Val Asp Ser Ser Val
131 180 185 190
132 Ala Ala Tyr Ser Met Arg Cys Ile Ser
133 195 200
135 <210> SEQ ID NO: 3
136 <211> LENGTH: 2943
137 <212> TYPE: DNA
138 <213> ORGANISM: Helianthus annuus
140 <220> FEATURE:
141 <221> NAME/KEY: misc_feature
142 <222> LOCATION: (0)...(0)
143 <223> OTHER INFORMATION: lox cDNA
145 <221> NAME/KEY: CDS
146 <222> LOCATION: (18)...(2720)
148 <400> SEQUENCE: 3
149 ggcacgagaa gaaaacc atg ttg aat tct caa atc aac cat tct cac cct 50
150 Met Leu Asn Ser Gln Ile Asn His Ser His Pro
151 1 5 10
153 ctt aac aac cta cta cca atc cgc aaa gcc ttt gtc cat ggt gac acc 98
154 Leu Asn Asn Leu Leu Pro Ile Arg Lys Ala Phe Val His Gly Asp Thr
155 15 20 25
157 act aac cat tcc tcc tcc aac gcc tac tcc ccc gcc aac ctt cgc caa 146
158 Thr Asn His Ser Ser Ser Asn Ala Tyr Ser Pro Ala Asn Leu Arg Gln
159 30 35 40
161 cac gcg tcc acc aag aaa tcc aat gct acc cgt gca cga tcc acc tca 194
162 His Ala Ser Thr Lys Lys Ser Asn Ala Thr Arg Ala Arg Ser Thr Ser
163 45 50 55
165 act gcg ggt aac att aaa gcc ata tca atc ccc ttt ctt acc aag gag 242
166 Thr Ala Gly Asn Ile Lys Ala Ile Ser Ile Pro Phe Leu Thr Lys Glu
167 60 65 70 75
169 acc acc gtc aag tgt gtc atc acc gtc caa cca acc att agt tcc gcc 290
170 Thr Thr Val Lys Cys Val Ile Thr Val Gln Pro Thr Ile Ser Ser Ala
171 80 85 90
173 att gct ggt gta gcc gtt ggt ggt att gtt gat ggt gtt tct aat ctt 338
174 Ile Ala Gly Val Gly Val Gly Gly Ile Val Asp Gly Val Ser Asn Leu
175 95 100 105
177 cta ggg ttg tca ttt ttg ttg gag ctg gtt tca aat gac ctg gat tca 386
178 Leu Gly Leu Ser Phe Leu Leu Glu Leu Val Ser Asn Asp Leu Asp Ser
179 110 115 120
181 aaa gga aac caa aag aca gtg aag gct tat gca aga tac aac gca ctg 434
182 Lys Gly Asn Gln Lys Thr Val Lys Ala Tyr Ala Arg Tyr Asn Ala Leu
183 125 130 135
185 gat ttg gac att agc gtg tac aca tac aaa tgc gac ttc gac gtc cct 482
186 Asp Leu Asp Ile Ser Val Tyr Thr Tyr Lys Cys Asp Phe Asp Val Pro
187 140 145 150 155

```

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189	gaa gat ttt ggg gag ata gga gct gtg ttg gta gaa aat gag tat agc	530
190	Glu Asp Phe Gly Glu Ile Gly Ala Val Leu Val Glu Asn Glu Tyr Ser	
191	160 165 170	
193	aag aag atg ttt ttc aag aac att gtt ctt aac aac ggt gtt acc ttc	578
194	Lys Lys Met Phe Phe Lys Asn Ile Val Leu Asn Asn Gly Val Thr Phe	
195	175 180 185	
197	aca tgc gag tca tgg gtt cac tcc aaa tac gat aac cct gag aaa aga	626
198	Thr Cys Glu Ser Trp Val His Ser Lys Tyr Asp Asn Pro Glu Lys Arg	
199	190 195 200	
201	ata ttt ttc acc gac aag tgc tat cta ccg ttg gaa acg ccg acg gca	674
202	Ile Phe Phe Thr Asp Lys Ser Tyr Leu Pro Leu Glu Thr Pro Thr Ala	
203	205 210 215	
205	ctg aag ccg tta cga gag aaa gat atg gaa tgc ctt cga gga aac ggc	722
206	Leu Lys Pro Leu Arg Glu Lys Asp Met Glu Ser Leu Arg Gly Asn Gly	
207	220 225 230 235	
209	gaa gga gaa cgt aaa tca ttc gag ccg ata tat gat tat gat gtg tac	770
210	Glu Gly Glu Arg Lys Ser Phe Glu Arg Ile Tyr Asp Tyr Asp Val Tyr	
211	240 245 250	
213	aac gat ctc gga gat ccg gat gga agc tta gat cta gca ccg ccg gtg	818
214	Asn Asp Leu Gly Asp Pro Asp Gly Ser Leu Asp Leu Ala Arg Pro Val	
215	255 260 265	
217	ctc ggt ggc gag aca cat ccg tac cct agc ccg tgc cgt act ggt cgc	866
218	Leu Gly Gly Glu Thr His Pro Tyr Pro Arg Arg Cys Arg Thr Gly Arg	
219	270 275 280	
221	aaa atg tcc tct aaa gat ccg tta aca gaa agc aga act acg ctc cct	914
222	Lys Met Ser Ser Lys Asp Pro Leu Thr Glu Ser Arg Thr Thr Leu Pro	
223	285 290 295	
225	ttt tat gta cct gcg gat gaa gat ttt tca gag ata aag agt gtg aac	962
226	Phe Tyr Val Pro Ala Asp Glu Asp Phe Ser Glu Ile Lys Ser Val Asn	
227	300 305 310 315	
229	ttt gga gca aaa act tta tac tct gtg ctt cat gga gtt gta cca atg	1010
230	Phe Gly Ala Lys Thr Leu Tyr Ser Val Leu His Gly Val Val Pro Met	
231	320 325 330	
233	cta gac tca att gta aca gac aaa gac aag ggg ttt cca tta ttc aca	1058
234	Leu Asp Ser Ile Val Thr Asp Lys Asp Lys Gly Phe Pro Leu Phe Thr	
235	335 340 345	
237	tcc ata gat ttg ctt tat aat gaa ggt gtt aat gtt cct tct cct gac	1106
238	Ser Ile Asp Leu Leu Tyr Asn Glu Gly Val Asn Val Pro Ser Pro Asp	
239	350 355 360	
241	aat gga att cta agt gct tta cct aga ctt gtc aaa ggg gct act gat	1154
242	Asn Gly Ile Leu Ser Ala Leu Pro Arg Leu Val Lys Gly Ala Thr Asp	
243	365 370 375	
245	gcc gca aat acc gtt atc aag ttc gag acc ccc gaa acc att gat aga	1202
246	Ala Ala Asn Thr Val Ile Lys Phe Glu Thr Pro Glu Thr Ile Asp Arg	
247	380 385 390 395	
249	gac gca ttc tca tgg ttc cgt gat gaa gag ttc tgc ccg caa atg ctt	1250
250	Asp Ala Phe Ser Trp Phe Arg Asp Glu Glu Phe Cys Arg Gln Met Leu	
251	400 405 410	
253	gcc ggt att aat cct tgt cgc ata caa ttg gtt acg gaa tgg cca ttg	1298

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Input Set : A:\Seqlist.txt

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254 Ala Gly Ile Asn Pro Cys Arg Ile Gln Leu Val Thr Glu Trp Pro Leu
255          415          420          425
257 atg agt aaa ctg gac cct gaa atc tat gga cca gct gag tca gca att 1346
258 Met Ser Lys Leu Asp Pro Glu Ile Tyr Gly Pro Ala Glu Ser Ala Ile
259          430          435          440
261 aca aag gag att gta gag gaa gag att aaa ggt ttc atg act ctt gag 1394
262 Thr Lys Glu Ile Val Glu Glu Glu Ile Lys Gly Phe Met Thr Leu Glu
263          445          450          455
265 gag gct tta gca caa aag aag ctg ttt atg ctg gat tat cat gat ctg 1442
266 Glu Ala Leu Ala Gln Lys Lys Leu Phe Met Leu Asp Tyr His Asp Leu
267 460          465          470          475
269 ctc ttg cct tat gtt aac aaa acg gag gct gaa ggg aga act ttg tat 1490
270 Leu Leu Pro Tyr Val Asn Lys Thr Glu Ala Glu Gly Arg Thr Leu Tyr
271          480          485          490
273 ggt tca aga act tta atg ttc ctt act cct gct gga aca tta agg cca 1538
274 Gly Ser Arg Thr Leu Met Phe Leu Thr Pro Ala Gly Thr Leu Arg Pro
275          495          500          505
277 cta gcc att gag ctg act cgc cca cca att gat ggg aaa cca cag tgg 1586
278 Leu Ala Ile Glu Leu Thr Arg Pro Pro Ile Asp Gly Lys Pro Gln Trp
279          510          515          520
281 aaa cat gtt tac aca ccc gct tgg gat gct aca ggt gca tgg ctt tgg 1634
282 Lys His Val Tyr Thr Pro Ala Trp Asp Ala Thr Gly Ala Trp Leu Trp
283          525          530          535
285 aag cta gcc aag gct cat gtc ctt gcc cat gat tct agc tat cac caa 1682
286 Lys Leu Ala Lys Ala His Val Leu Ala His Asp Ser Ser Tyr His Gln
287 540          545          550          555
289 ctt gtt agc cat tgg cta aga aca cat tgt gct acc gaa cct tac att 1730
290 Leu Val Ser His Trp Leu Arg Thr His Cys Ala Thr Glu Pro Tyr Ile
291          560          565          570
293 att gct acc aat cgc caa ctc agt caa atg cat cca att cga cga ttt 1778
294 Ile Ala Thr Asn Arg Gln Leu Ser Gln Met His Pro Ile Arg Arg Phe
295          575          580          585
297 cta ctc cct cac ttt cgt tac act atg caa att aat tct cta gct aga 1826
298 Leu Leu Pro His Phe Arg Tyr Thr Met Gln Ile Asn Ser Leu Ala Arg
299          590          595          600
301 ctt tta ctc gtc aat gcc atg ggt atc ata gag tca aca ttt tct cct 1874
302 Leu Leu Leu Val Asn Ala Met Gly Ile Ile Glu Ser Thr Phe Ser Pro
303          605          610          615
305 gga aga tat tgt atg caa att tcc tct gat gca tat gat cag caa tgg 1922
306 Gly Arg Tyr Cys Met Gln Ile Ser Ser Asp Ala Tyr Asp Gln Gln Trp
307 620          625          630          635
309 cgt ttt gat cat gaa gcg ctt ccg gcc gac cta att agc agg ggt atg 1970
310 Arg Phe Asp His Glu Ala Leu Pro Ala Asp Leu Ile Ser Arg Gly Met
311          640          645          650
313 gcg gtt gaa gat cca acc gca cca tat ggt gta aaa cta aca atc gag 2018
314 Ala Val Glu Asp Pro Thr Ala Pro Tyr Gly Val Lys Leu Thr Ile Glu
315          655          660          665
317 gat tac cca tat gca aat gah ggt tta ctc att tat gat acc att aaa 2066
318 Asp Tyr Pro Tyr Ala Asn Asp Gly Leu Leu Ile Tyr Asp Thr Ile Lys

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VERIFICATION SUMMARY                      DATE: 12/01/2000  
PATENT APPLICATION: US/09/714,767        TIME: 13:32:15

Input Set : A:\Seqlist.txt  
Output Set: N:\CRF3\12012000\I714767.raw

L:18 M:270 C: Current Application Number differs, Replaced Current Application No  
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date